

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/941,095
Source: OIPE
Date Processed by STIC: 11/29/2005

ENTERED



OIPE

RAW SEQUENCE LISTING

DATE: 11/29/2005

PATENT APPLICATION: US/09/941,095

TIME: 15:58:42

Input Set : N:\Crif3\RULE60\09941095.raw

Output Set: N:\CRF4\11292005\I941095.raw

SEQUENCE LISTING

```

1 (1) GENERAL INFORMATION:
2   (i) APPLICANT: BROW, MARY ANN D.
3             LYAMICHEV, VICTOR I.
4             OLIVE, DAVID M.
5   (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
6             PATHOGENS
7   (iii) NUMBER OF SEQUENCES: 165
8   (iv) CORRESPONDENCE ADDRESS:
9         (A) ADDRESSEE: MEDLEN & CARROLL
10        (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
11        (C) CITY: SAN FRANCISCO
12        (D) STATE: CALIFORNIA
13        (E) COUNTRY: UNITED STATES OF AMERICA
14        (F) ZIP: 94104
15   (v) COMPUTER READABLE FORM:
16        (A) MEDIUM TYPE: Floppy disk
17        (B) COMPUTER: IBM PC compatible
18        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
19        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
20   (vi) CURRENT APPLICATION DATA:
C--> 21        (A) APPLICATION NUMBER: US/09/941,095
C--> 22        (B) FILING DATE: 28-Aug-2001
W--> 27        (C) CLASSIFICATION:
24   (vii) PRIOR APPLICATION DATA:
25        (A) APPLICATION NUMBER: US/09/941,193
26        (B) FILING DATE: 28-Aug-2001
28   (viii) ATTORNEY/AGENT INFORMATION:
29        (A) NAME: CARROLL, PETER G.
30        (B) REGISTRATION NUMBER: 32,837
31        (C) REFERENCE/DOCKET NUMBER: FORS-01756
32   (ix) TELECOMMUNICATION INFORMATION:
33        (A) TELEPHONE: (415) 705-8410
34        (B) TELEFAX: (415) 397-8338
35 (2) INFORMATION FOR SEQ ID NO: 1:
36   (i) SEQUENCE CHARACTERISTICS:
37        (A) LENGTH: 2506 base pairs
38        (B) TYPE: nucleic acid
39        (C) STRANDEDNESS: double
40        (D) TOPOLOGY: linear
41   (ii) MOLECULE TYPE: DNA (genomic)
42   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
43   ATGAGGGGGA TGCTGCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC

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60

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44 CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG 120
45 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC 180
46 GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCTCCTTCC GCCACGAGGC CTACGGGGGG 240
47 TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG 300
48 GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTCGAGGTCC CGGGCTACGA GGCGGACGAC 360
49 GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG CATCCTCACC 420
50 GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCTCCA CCCCAGGGGG 480
51 TACCTCATCA CCCCAGCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCCG CCAGTGGGCC 540
52 GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA GGGCATCGGG 600
53 GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGAAGCCCT CCTCAAGAAC 660
54 CTGGACCGG TGAAGCCCGC CATCCGGGAG AAGATCCTGG CCCACATGGA CGATCTGAAG 720
55 CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCC TGGAGGTGGA CTTGCGCCAA 780
56 AGGCGGGAGC CCGACGGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA GTTTGGCAGC 840
57 CTCCTCCACG AGTTCCGGCT TCTGGAAAGC CCCAAGGCC TGGAGGAGGC CCCCCTGGCCC 900
58 CCGCCGGAAG GGGCCTTCGT GGGCTTTGTG CTTTCCCGCA AGGAGCCCAT GTGGGCGCAT 960
59 CTTCTGGCCC TGGCCCGCGC CAGGGGGGGC CGGGTCCACC GGGCCCCCGA GCCTTATAAA 1020
60 GCCCTCAGGG ACCTGAAGGA GGCGCGGGG CTTCTCGCCA AAGACCTGAG CGTTCTGGCC 1080
61 CTGAGGGAAG GCCTTGGCCT CCCGCCCGC GACGACCCA TGCTCCTCGC CTACCTCCTG 1140
62 GACCCTTCCA ACACACCCC CGAGGGGGTG GCCCGCGCT ACGGCGGGGA GTGGACGGAG 1200
63 GAGGCGGGG AGCGGGCCG CCTTTCCGAG AGGCTCTTCG CCAACCTGTG GGGGAGGCTT 1260
64 GAGGGGGAGG AGAGGCTCCT TTGGCTTTAC CGGGAGGTGG AGAGGCCCCC TTCCGCTGTC 1320
65 CTGGCCACA TGGAGGCCAC GGGGGTGCGC CTGGACGTGG CCTATCTCAG GGCCTTGTCC 1380
66 CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAGG TCTTCCGCCT GGCCGGCCAC 1440
67 CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT 1500
68 CCCGCCATCG GCAAGACGGA GAAGACCGG AAGCGCTCCA CCAGCGCCG CGTCTGGAG 1560
69 GCCCTCCGCG AGGCCCACCC CATCGTGGAG AAGATCCTGC AGTACCGGGA GCTCACCAAG 1620
70 CTGAAGAGCA CCTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC GGGCCGCCTC 1680
71 CACACCGCT TCAACAGAC GGCCACGGC ACGGGCAGG TAAGTAGCTC CGATCCCAAC 1740
72 CTCCAGAACA TCCCCGTCCG CACCCCGCTT GGGCAGAGGA TCCGCCGGC CTTTCATCGC 1800
73 GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC 1860
74 CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGGCGGGA CATCCACACG 1920
75 GAGACGCCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCCT GATGCGCCGG 1980
76 GCGGCCAAGA CCATCAACTT CGGGGTCTC TACGGCATGT CGGCCACCG CCTCTCCAG 2040
77 GAGCTAGCCA TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC 2100
78 CCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG 2160
79 GAGACCCTCT TCGGCCGCG CCGTACGTG CCAGACCTAG AGGCCGGGT GAAGAGCGTG 2220
80 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCGTCC AGGCCACGC CGCCGACCTC 2280
81 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGG CAGGATGCTC 2340
82 CTTCAGGTCC ACGACGAGCT GGTCTTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 2400
83 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCTGG CCGTGCCCCCT GGAGGTGGAG 2460
84 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 2506

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86 (2) INFORMATION FOR SEQ ID NO: 2:

87 (i) SEQUENCE CHARACTERISTICS:

88 (A) LENGTH: 2496 base pairs

89 (B) TYPE: nucleic acid

90 (C) STRANDEDNESS: double

91 (D) TOPOLOGY: linear

92 (ii) MOLECULE TYPE: DNA (genomic)

93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

RAW SEQUENCE LISTING

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Input Set : N:\Crif3\RULE60\09941095.raw

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94	ATGGCGATGC TTCCCTCTT TGAGCCCAA GGC CGGTGC TCCTGGTGA CGGCCACCAC	60
95	CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT	120
96	CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCC TGAAGGAGGA CGGGGACGTG	180
97	GTGGTGGTGG TCTTTGACGC CAAGGCCCC TCCTTCCGCC ACGAGGCC TA CGAGGCCCTAC	240
98	AAGGCGGGCC GGGCCCCC CCGGAGGAC TTTCCCCGGC AGCTGGCCCT CATCAAGGAG	300
99	TTGGTGGACC TCCTAGGCC TGTGCGGCTG GAGGTTCCCG GCTTTGAGGC GGACGACGTG	360
100	CTGGCCACCC TGGCCAAGCG GGC GAAAG GAGGGGTACG AGGTGCGCAT CCTCACTGCC	420
101	GACCGCGACC TCTACCAGCT CCTTTCGGAG CGCATCGCCA TCCTCCACCC TGAGGGGTAC	480
102	CTGATCACCC CGGCGTGGCT TTACGAGAA TACGGCCTGC GCCCGGAGCA GTGGGTGGAC	540
103	TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGTGGAAGGG CATCGGGGAG	600
104	AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG	660
105	GACCAGGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCGG GCATGGAGGC CCTGGCCCTT	720
106	TCCCGAAGC TTTCCAGGT GCACACTGAC CTGCCCTGG AGGTGGACTT CGGGAGGCGC	780
107	CGCACACCA ACCTGGAGGG TCTGCGGGCT TTTTGGAGC GGTGGAGTT TGAAGCCTC	840
108	CTCCACGAGT TCGGCCTCCT GGAGGGGCGG AAGGCGGCAG AGGAGGCCCT CTGGCCCCCT	900
109	CCGGAAGGGG CTTTTTTGGG CTTTTCTTT TCCCGTCCCG AGCCCATGTG GGCCGAGCTT	960
110	CTGGCCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC	1020
111	CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG	1080
112	CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC	1140
113	CCCTCCAACA CCACCCCTGA GGGGTGGCC CGGCGTTACG GGGGGAGTG GACGGAGGAT	1200
114	GCGGGGAGA GGGCCCTCCT GCGGAGCGC CTCTTCAGA CCCTAAAGGA GCGCTTAAG	1260
115	GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGTGTTG	1320
116	GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG	1380
117	GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC	1440
118	TTCAACCTCA ACTCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT	1500
119	GCCATCGGCA AGACGGAGAA GACGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC	1560
120	CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCTGCAGT ACCGGGAGCT CACCAAGCTC	1620
121	AAGAACCTT ACATAGACCC CTGCCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC	1680
122	ACCCGCTTCA ACCAGACGGC CACCGCCAG GGCAGGCTTT CCAGCTCCGA CCCAACCTG	1740
123	CAGAACATCC CCGTGCGCAC CCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG	1800
124	GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCAC	1860
125	CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG	1920
126	ACCGCCAGCT GGATGTTCCG CGTTTCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG	1980
127	GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG	2040
128	CTTTCCATCC CCTACGAGGA GCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC	2100
129	AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG	2160
130	ACCCTCTTCG GCCGCCGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGC GC	2220
131	GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG	2280
132	AAGCTGGCCA TGGTGC GGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG	2340
133	CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCAAGGACC GGGCGGAGAG GGTAGCCGCT	2400
134	TTGGCCAAGG AGGTCATGGA GGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG	2460
135	GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG	2496

137 (2) INFORMATION FOR SEQ ID NO: 3:

138 (i) SEQUENCE CHARACTERISTICS:

139 (A) LENGTH: 2504 base pairs

140 (B) TYPE: nucleic acid

141 (C) STRANDEDNESS: double

142 (D) TOPOLOGY: linear

143 (ii) MOLECULE TYPE: DNA (genomic)

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144 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
145 ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC 60
146 CACCTGGCCT ACCGCACCTT CTTGCCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG 120
147 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCTCAAGG CCTGAAGGA GGACGGGTAC 180
148 AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCTACGAG 240
149 GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC 300
150 AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCTCGAGG TCCCCGGCTA CGAGGCGGAC 360
151 GACGTTCTCG CCACCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC 420
152 ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCTT CCACCCCGAG 480
153 GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG 540
154 GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC 600
155 GGGGAGAAGA GCGCCCTCAA GCTCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG 660
156 AACCTGGACC GGTAAAGCC AGAAACGTC CGGAGAAGA TCAAGGCCCA CTTGGAAGAC 720
157 CTCAGGCTCT CTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC 780
158 GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC 840
159 GGCAGCTTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC 900
160 TGGCCCCCGC CGGAAGGGGC CTTGCTGGGC TTCGTCCTCT CCCGCCCCGA GCCCATGTGG 960
161 GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC 1020
162 TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC 1080
163 TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCATGCT CCTCGCCTAC 1140
164 CTCTGGACC CCTCCAACAC CACCCCGAG GGGGTGGCGC GCGCTACGG GGGGGAGTGG 1200
165 ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG 1260
166 CGCCTCGAGG GGGAGGAGAA GTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC 1320
167 CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC 1380
168 CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG 1440
169 GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAG GGGTGCTCTT TGACGAGCTT 1500
170 AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG 1560
171 CTGGAGGCCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC 1620
172 ACCAAGCTCA AGAACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC 1680
173 CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC 1740
174 CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC 1800
175 GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC 1860
176 CTCGCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC 1920
177 CACACCAGA CCGCAAGCTG GATGTTCCGC GTCCCCCGG AGGCCGTGGA CCCCTGATG 1980
178 CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
179 TCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
180 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT 2160
181 ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
182 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG 2280
183 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCCT CCGGGAGATG GGGGCCCCGA 2340
184 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400
185 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG 2460
186 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

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188 (2) INFORMATION FOR SEQ ID NO: 4:

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189 (i) SEQUENCE CHARACTERISTICS:
190 (A) LENGTH: 832 amino acids
191 (B) TYPE: amino acid
192 (C) STRANDEDNESS: single
193 (D) TOPOLOGY: linear

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194 (ii) MOLECULE TYPE: protein
195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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197 1 5 10 15
198 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
199 20 25 30
200 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
201 35 40 45
202 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
203 50 55 60
204 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
205 65 70 75 80
206 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
207 85 90 95
208 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
209 100 105 110
210 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
211 115 120 125
212 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
213 130 135 140
214 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
215 145 150 155 160
216 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
217 165 170 175
218 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
219 180 185 190
220 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
221 195 200 205
222 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
223 210 215 220
224 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
225 225 230 235 240
226 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
227 245 250 255
228 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
229 260 265 270
230 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
231 275 280 285
232 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
233 290 295 300
234 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
235 305 310 315 320
236 Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
237 325 330 335
238 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
239 340 345 350
240 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
241 355 360 365
242 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 11/29/2005

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TIME: 15:58:43

Input Set : N:\Cr3\RULE60\09941095.raw

Output Set: N:\CRF4\11292005\I941095.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 4,5,181,182,190,366,617,628,685,714,722,738,784,1022,1029

Seq#:7; N Pos. 1038,1053,1098,1105,1206,1227,1244,1251,1252,1253,1350,1380

Seq#:7; N Pos. 1497,1530,1569,1572,1641,1653,1655,1770,1812,2319,2346,2396

Seq#:8; Xaa Pos.2,63,109,186,205,209,227,228,233,240,243,244,247,260,290

Seq#:8; Xaa Pos.329,336,340,368,414,417,418,431,551,605,773,794,798,823,833

VERIFICATION SUMMARY

DATE: 11/29/2005

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Input Set : N:\Crf3\RULE60\09941095.raw

Output Set: N:\CRF4\11292005\I941095.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:176
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:192
L:748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:208
L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:240
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256
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L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:320
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:336
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L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592
L:818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:768
L:820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:784
L:824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:816
L:826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:832